

Figure 6. The effect of the number of iterations on the accuracy of the proposed algorithm. The results are shown for different values of α and β . The x-axis represents the number of iterations (0 to 100), and the y-axis represents the accuracy (0.8 to 1.0). The legend indicates four cases: $(\alpha=0.9, \beta=0.9)$, $(\alpha=0.9, \beta=0.7)$, $(\alpha=0.7, \beta=0.9)$, and $(\alpha=0.7, \beta=0.7)$.

400> 1	atg	acg	tcc	gtt	aac	gtt	aag	ctc	ctt	tac	cgt	tac	gtc	tta	acc	aac	48
Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn		
1				5					10					15			
	ttt	ttc	aac	ctc	tgt	ttg	ttc	ccg	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys		
			20					25					30				
	gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
			35					40					45				
	caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	gtt	ttc	192
Gln	His	Asn	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
			50				55					60					
	ggt	ttg	gtt	ctc	tac	atc	gta	acc	cga	ccc	aat	ccg	gtt	tat	ctc	gtt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val		
65					70					75				80			
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Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	
				85						90					95		
	aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
			100					105					110				
	cgg	aac	gtg	gca	tgt	gat	gat	ccg	tcc	tcg	ctc	gat	ttc	ctg	agg	aag	384

[illegible]

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 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
 355 360 365

cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct 1152
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag 1200
 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
 385 390 395 400

cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga 1248
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt 1392
 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa 1440
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
 465 470 475 480

cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
 485 490 495

tca aag act cat gtc caa aac ggt cgg tcc taatttgatg tatctgagtg 1538
 Ser Lys Thr His Val Gln Asn Gly Arg Ser
 500 505

ccaacgttta ctttgtcttt cctttctttt attggttatg aattagatgt ttactaatgt 1598
 tcctctcttt ttcgttataa ataaagaagt tcaattcttc ctatagtttc aaacgcgatt 1658
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 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu

[illegible]

<213> Brassica napus

 $\langle 222 \rangle \quad (1) \dots (1521)$

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Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
20 25 30

gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat 144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
35 40 45

ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt 192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
50 55 60

ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa cgg gtt tac ctc 240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
65 70 75 80

ggt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc 288
Val Glu Tyr Ser Cys Tyr Leu Pro Thr His Cys Arg Ser Ser Ile
85 90 95

tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct 336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
100 105 110

cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag 384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
115 120 125

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
130 135 140

ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag 480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
145 150 155 160

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc 528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
165 170 175

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in YEA medium for 24 h at 28 °C. The cell concentration of the strains was adjusted to 10⁸ cells/ml. The cell suspension was then diluted to 10⁶, 10⁷, 10⁸, 10⁹, 10¹⁰, 10¹¹, 10¹², 10¹³, 10¹⁴, 10¹⁵, 10¹⁶, 10¹⁷, 10¹⁸, 10¹⁹, 10²⁰, 10²¹, 10²², 10²³, 10²⁴, 10²⁵, 10²⁶, 10²⁷, 10²⁸, 10²⁹, 10³⁰, 10³¹, 10³², 10³³, 10³⁴, 10³⁵, 10³⁶, 10³⁷, 10³⁸, 10³⁹, 10⁴⁰, 10⁴¹, 10⁴², 10⁴³, 10⁴⁴, 10⁴⁵, 10⁴⁶, 10⁴⁷, 10⁴⁸, 10⁴⁹, 10⁵⁰, 10⁵¹, 10⁵², 10⁵³, 10⁵⁴, 10⁵⁵, 10⁵⁶, 10⁵⁷, 10⁵⁸, 10⁵⁹, 10⁶⁰, 10⁶¹, 10⁶², 10⁶³, 10⁶⁴, 10⁶⁵, 10⁶⁶, 10⁶⁷, 10⁶⁸, 10⁶⁹, 10⁷⁰, 10⁷¹, 10⁷², 10⁷³, 10⁷⁴, 10⁷⁵, 10⁷⁶, 10⁷⁷, 10⁷⁸, 10⁷⁹, 10⁸⁰, 10⁸¹, 10⁸², 10⁸³, 10⁸⁴, 10⁸⁵, 10⁸⁶, 10⁸⁷, 10⁸⁸, 10⁸⁹, 10⁹⁰, 10⁹¹, 10⁹², 10⁹³, 10⁹⁴, 10⁹⁵, 10⁹⁶, 10⁹⁷, 10⁹⁸, 10⁹⁹, 10¹⁰⁰, 10¹⁰¹, 10¹⁰², 10¹⁰³, 10¹⁰⁴, 10¹⁰⁵, 10¹⁰⁶, 10¹⁰⁷, 10¹⁰⁸, 10¹⁰⁹, 10¹¹⁰, 10¹¹¹, 10¹¹², 10¹¹³, 10¹¹⁴, 10¹¹⁵, 10¹¹⁶, 10¹¹⁷, 10¹¹⁸, 10¹¹⁹, 10¹²⁰, 10¹²¹, 10¹²², 10¹²³, 10¹²⁴, 10¹²⁵, 10¹²⁶, 10¹²⁷, 10¹²⁸, 10¹²⁹, 10¹³⁰, 10¹³¹, 10¹³², 10¹³³, 10¹³⁴, 10¹³⁵, 10¹³⁶, 10¹³⁷, 10¹³⁸, 10¹³⁹, 10¹⁴⁰, 10¹⁴¹, 10¹⁴², 10¹⁴³, 10¹⁴⁴, 10¹⁴⁵, 10¹⁴⁶, 10¹⁴⁷, 10¹⁴⁸, 10¹⁴⁹, 10¹⁵⁰, 10¹⁵¹, 10¹⁵², 10¹⁵³, 10¹⁵⁴, 10¹⁵⁵, 10¹⁵⁶, 10¹⁵⁷, 10¹⁵⁸, 10¹⁵⁹, 10¹⁶⁰, 10¹⁶¹, 10¹⁶², 10¹⁶³, 10¹⁶⁴, 10¹⁶⁵, 10¹⁶⁶, 10¹⁶⁷, 10¹⁶⁸, 10¹⁶⁹, 10¹⁷⁰, 10¹⁷¹, 10¹⁷², 10¹⁷³, 10¹⁷⁴, 10¹⁷⁵, 10¹⁷⁶, 10¹⁷⁷, 10¹⁷⁸, 10¹⁷⁹, 10¹⁸⁰, 10¹⁸¹, 10¹⁸², 10¹⁸³, 10¹⁸⁴, 10¹⁸⁵, 10¹⁸⁶, 10¹⁸⁷, 10¹⁸⁸, 10¹⁸⁹, 10¹⁹⁰, 10¹⁹¹, 10¹⁹², 10¹⁹³, 10¹⁹⁴, 10¹⁹⁵, 10¹⁹⁶, 10¹⁹⁷, 10¹⁹⁸, 10¹⁹⁹, 10²⁰⁰, 10²⁰¹, 10²⁰², 10²⁰³, 10²⁰⁴, 10²⁰⁵, 10²⁰⁶, 10²⁰⁷, 10²⁰⁸, 10²⁰⁹, 10²¹⁰, 10²¹¹, 10²¹², 10²¹³, 10²¹⁴, 10²¹⁵, 10²¹⁶, 10²¹⁷, 10²¹⁸, 10²¹⁹, 10²²⁰, 10²²¹, 10²²², 10²²³, 10²²⁴, 10²²⁵, 10²²⁶, 10²²⁷, 10²²⁸, 10²²⁹, 10²³⁰, 10²³¹, 10²³², 10²³³, 10²³⁴, 10²³⁵, 10²³⁶, 10²³⁷, 10²³⁸, 10²³⁹, 10²⁴⁰, 10²⁴¹, 10²⁴², 10²⁴³, 10²⁴⁴, 10²⁴⁵, 10²⁴⁶, 10²⁴⁷, 10²⁴⁸, 10²⁴⁹, 10²⁵⁰, 10²⁵¹, 10²⁵², 10²⁵³, 10²⁵⁴, 10²⁵⁵, 10²⁵⁶, 10²⁵⁷, 10²⁵⁸, 10²⁵⁹, 10²⁶⁰, 10²⁶¹, 10²⁶², 10²⁶³, 10²⁶⁴, 10²⁶⁵, 10²⁶⁶, 10²⁶⁷, 10²⁶⁸, 10²⁶⁹, 10²⁷⁰, 10²⁷¹, 10²⁷², 10²⁷³, 10²⁷⁴, 10²⁷⁵, 10²⁷⁶, 10²⁷⁷, 10²⁷⁸, 10²⁷⁹, 10²⁸⁰, 10²⁸¹, 10²⁸², 10²⁸³, 10²⁸⁴, 10²⁸⁵, 10²⁸⁶, 10²⁸⁷, 10²⁸⁸, 10²⁸⁹, 10²⁹⁰, 10²⁹¹, 10²⁹², 10²⁹³, 10²⁹⁴, 10²⁹⁵, 10²⁹⁶, 10²⁹⁷, 10²⁹⁸, 10²⁹⁹, 10³⁰⁰, 10³⁰¹, 10³⁰², 10³⁰³, 10³⁰⁴, 10³⁰⁵, 10³⁰⁶, 10³⁰⁷, 10³⁰⁸, 10³⁰⁹, 10³¹⁰, 10³¹¹, 10³¹², 10³¹³, 10³¹⁴, 10³¹⁵, 10³¹⁶, 10³¹⁷, 10³¹⁸, 10³¹⁹, 10³²⁰, 10³²¹, 10³²², 10³²³, 10³²⁴, 10³²⁵, 10³²⁶, 10³²⁷, 10³²⁸, 10³²⁹, 10³³⁰, 10³³¹, 10³³², 10³³³, 10³³⁴, 10³³⁵, 10³³⁶, 10³³⁷, 10³³⁸, 10³³⁹, 10³⁴⁰, 10³⁴¹, 10³⁴², 10³⁴³, 10³⁴⁴, 10³⁴⁵, 10³⁴⁶, 1

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 420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tgg aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
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Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45

Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
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Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80

Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95

Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
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Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
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Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
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Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160

Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175

Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met

180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
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 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
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 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
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 385 390 395 400
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 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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 Met Thr Ser Ile Asn Val Lys Leu Leu
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[illegible]

460

465

470

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 475 480 485

gat tct gat tca ggt aag tca gag act cgt gtc cca aac ggt cgg tcc 1599
 Asp Ser Asp Ser Gly Lys Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 490 495 500 505

taataaatga tgtttgctct ctttcgtttc tttttattgg ttataataat ttgatggcca 1659
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 Ala Tyr Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Ile Ala Pro Leu Leu Ala Phe Thr Val Phe
 50 55 60
 Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu Val
 65 70 75 80
 Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser
 85 90 95
 Lys Val Met Asp Ile Phe Phe Gln Val Arg Lys Ala Asp Pro Ser Arg
 100 105 110
 Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile
 115 120 125
 Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu
 130 135 140
 Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Arg Ala Arg Glu Glu Thr
 145 150 155 160
 Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn
 165 170 175
 Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
 180 185 190
 Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu
 195 200 205
 Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
 210 215 220
 Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
 225 230 235 240
 Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile
 245 250 255
 Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
 260 265 270
 Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg Asp Arg Arg
 275 280 285
 Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala

Figure 10	Figure 11	Figure 12	Figure 13	Figure 14	Figure 15

<211> 1521

<213> Artificial Sequence

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NO:3); designated At114

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Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu

Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50 55 60

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80

gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct 288
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110

cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag 384
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140

ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag 480
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc 528
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175

aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg 576
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190

ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag 624
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205

ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt 672
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220

gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat 720
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240

aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac 768
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255

att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc 816
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270

cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt 864
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285

[illegible]

[illegible]

<223> 5' 114 amino acids from *A. thaliana* FAEl (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4); designated At114

[illegible]

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 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 9

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 222 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and
 3' 1296 bp from *B. napus* elongase KCS (SEQ ID
 NO:3); designated At74

<221> CDS

<222> (1)...(1515)

<400> 9

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 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

ggt ttg gtt ctc tac atc gta acc cga ccc aaa ccg gtt tac ctc gtt 240
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val
 65 70 75 80

009747E-050001

Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly	
305 310 315 320	
aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt cga	1008
Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg	
325 330 335	
acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg tta	1056
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu	
340 345 350	
agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt ttc	1104
Ser Glu Lys Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe	
355 360 365	
aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct att	1152
Lys Asp Lys Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile	
370 375 380	
gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg cta	1200
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu	
385 390 395 400	
gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga tca	1248
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser	
405 410 415	
acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat gag	1296
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr Glu	
420 425 430	
ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa gtt	1344
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val	
435 440 445	
tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt tgg	1392
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp	
450 455 460	
gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa cac	1440
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His	
465 470 475 480	
tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag tca	1488
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser	
485 490 495	
gag act cgt gtc caa aac ggt cgg tcc taa	1518
Glu Thr Arg Val Gln Asn Gly Arg Ser	
500 505	

<210> 10

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 74 amino acids from A. thaliana FAE1 (SEQ ID
NO:2) and 3' 431 amino acids from B. napus
elongase KCS (SEQ ID NO:4); designated At74

<400> 10

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Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
20      25      30
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
35      40      45
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50      55      60
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val
65      70      75
Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser
85      90      95
Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg
100     105     110
Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile
115     120     125
Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu
130     135     140
Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu Thr
145     150     155
Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn
165     170     175
Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
180     185     190
Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu
195     200     205
Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
210     215     220
Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
225     230     235
Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile
245     250     255
Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
260     265     270
Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg
275     280     285
Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala
290     295     300
Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly
305     310     315
Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg
325     330     335
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
340     345     350
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
355     360     365
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
370     375     380
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
385     390     395
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
400

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000711E-000001

[illegible]

400> 11																
atg	acg	tcc	gtt	aac	gtt	aag	ctc	ctt	tac	cgt	tat	gtc	tta	acc	aac	48
Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	
				5					10					15		
ttt	ttc	aac	ctc	tgt	ttg	ttc	cgg	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
				20					25					30		
gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
				35					40					45		
caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	gtt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
				50					55					60		
ggt	ttg	gtt	ctc	tac	atc	gta	acc	cga	ccc	aat	cgg	ggt	tat	ctc	ggt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
				65					70					75	80	
gac	tac	tcg	tgt	tac	ctt	cgg	cca	cgg	cat	tcg	aga	ggt	agt	gtc	tct	288
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Cys	Arg	Val	Ser	Val	Ser	
				85					90					95		
aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
				100					105					110		

cgg aac ggc acg tgt gat aat tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tgc ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056

000747E.000001

Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
340 345 350

tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt 1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
355 360 365

ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct 1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
370 375 380

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg 1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385 390 395 400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
405 410 415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
450 455 460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
485 490 495

tca gag act cgt gtc cca aac ggt cgg tcc taa 1521
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
500 505

<210> 12

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAEL (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4) having mutations at residues 91 and 92; designated At114 L91C K92R

<400> 12

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1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

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Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465                               470           475           480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
                               485           490           495
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
                    500                   505

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<210> 13
<211> 1521
<212> DNA
<213> Artificial Sequence

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<220>
<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
      3' 1179 bp from B. napus elongase KCS (SEQ ID
      NO:3), having a mutation at position 275;
      designated At114 K92R

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<221> CDS
<222> (1)...(1518)

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<400> 13
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Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1                               5                10                15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
                20                25                30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
                35                40                45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
                50                55                60

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt      240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
  65                70                75                80

gac tac tcg tgt tac ctt ccg cca ccg cat ctc aga gtt agt gtc tct      288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser
                85                90                95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca      336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
                100               105               110

cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag      384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
                115                120                125

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg      432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
                130                135                140

```


Abstract The purpose of this study was to determine the effect of a 12-week training program on the physical fitness of 10-year-old children. The study was conducted in a primary school in the city of Ankara, Turkey. The study group consisted of 20 children (10 boys and 10 girls) who were randomly selected from the 10-year-old children in the school. The children were divided into two groups: a control group and an experimental group. The control group did not participate in any physical activity program, while the experimental group participated in a 12-week training program. The physical fitness of the children was measured at the beginning and at the end of the 12-week period. The measurements included maximum heart rate, maximum oxygen consumption, maximum power, and maximum speed. The results of the study showed that the experimental group had significantly higher values for all four measurements at the end of the 12-week period compared to the control group. The results suggest that a 12-week training program can improve the physical fitness of 10-year-old children.

ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct 1152
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

att gac cat ttt tgt ata cat gcc gga gcc aga gcc gtg att gat gtg 1200
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

tca gag act cgt gtc cca aac ggt cgg tcc taa 1521
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 14

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 392 amino acids from B. napus
 elongase KCS (SEQ ID NO:4), having a mutation at
 position 92; designated At114 K92R

<400> 14

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
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 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

[illegible]

<210> 15
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3), having a mutation at position 920;
 designated At114 G307D; hypothetical

<221> CDS
 <222> (1)...(1518)

<400> 15
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 Met Thr Ser Val Asn Val Lys Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80

gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct 288
 Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110

cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag 384
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140

ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag 480
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu
 145 150 155 160

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc 528
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr

	165	170	175	
	aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			576
	180	185	190	
	ttt aat cca act cca tgc ctc tcc gcg atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			624
	195	200	205	
	ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			672
	210	215	220	
	gcc gcc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			720
	225	230	235	
	aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			768
	245	250	255	
	att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			816
	260	265	270	
	cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			864
	275	280	285	
	aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			912
	290	295	300	
	gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			960
	305	310	315	
	ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			1008
	325	330	335	
	cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			1056
	340	345	350	
	tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			1104
	355	360	365	
	ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			1152
	370	375	380	
	att gac cat ttt tgt ata cat gcc gga gcc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			1200
	385	390	395	
			400	

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tgg aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

tca gag act cgt gtc caa aac ggt cgg tcc taa 1521
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 16

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4) having mutation at residue 307; designated At114 G307D; hypothetical

<400> 16

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys

103000-5242500

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      115              120              125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
130              135              140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu
145              150              155              160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
165              170              175
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
180              185              190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
195              200              205
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
210              215              220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225              230              235              240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
245              250              255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
260              265              270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
275              280              285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
290              295              300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305              310              315              320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
325              330              335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
340              345              350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
355              360              365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
370              375              380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385              390              395              400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
405              410              415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
420              425              430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
435              440              445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
450              455              460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465              470              475              480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
485              490              495
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
500              505

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<210> 17

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and

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<221> CDS
<222> (1) . . . (1515)
```

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac 48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50 55 60

ggt ttg gtt ctc tac atc gta acc cga ccc aaa ccg gtt tac ctc gtt 240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val
65 70 75 80

gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc tcc 288
Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser
85 90 95

aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct cgg 336
Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg
100 105 110

aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag att 384
Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile
115 120 125

caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg ctg 432
Gln Glu Arg Ser Gly Leu Asp Glu Thr His Gly Pro Glu Gly Leu
130 135 140

ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag acg 480
Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu Thr
145 150 155 160

gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc aac 528
Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn
165 170 175

ggt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg ttt 576
Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
180 185 190

aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag ctc 624

[illegible]

Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	Leu	
	195						200					205				
cga	agc	aac	gta	aga	agc	ttt	aac	ctt	ggc	ggc	atg	ggc	tgt	agt	gcc	672
Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	
	210					215					220					
ggc	gtt	ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat	aaa	720
Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	Lys	
	225				230					235					240	
aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	att	768
Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	Ile	
			245						250					255		
tac	gct	ggc	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	cgt	816
Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	Arg	
			260				265						270			
gtt	ggc	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	aga	864
Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	Arg	
			275				280					285				
cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	gct	912
Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	Ala	
			290			295					300					
gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	ggc	960
Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	Gly	
	305				310					315					320	
aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggc	cga	1008
Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	Arg	
			325					330						335		
acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggc	ccg	ttg	att	ctt	ccg	tta	1056
Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	Leu	
			340					345					350			
agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	ttc	1104
Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	Phe	
			355			360						365				
aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	att	1152
Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	Ile	
	370					375					380					
gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg	cta	1200
Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	Leu	
	385				390					395					400	
gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga	tca	1248
Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	Ser	
			405					410						415		
acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tgg	tat	gag	1296
Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	Glu	

[illegible]

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 74 amino acids from *A. thaliana* FAEL (SEQ ID NO:2) and 3' 431 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having a mutation at residue 306; designated At74 G306D; hypothetical

<400> 18

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5				10					15		
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
			20					25				30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
			35				40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
			50				55				60				
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	Val
65				70						75				80	
Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	Ser
			85							90				95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	Arg
			100					105					110		
Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	Ile
			115				120					125			
Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	Leu
			130				135				140				
Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	Thr
145					150				155					160	
Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	Asn
			165						170					175	

Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
 180 185 190
 Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu
 195 200 205
 Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
 210 215 220
 Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
 225 230 235 240
 Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile
 245 250 255
 Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
 260 265 270
 Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg
 275 280 285
 Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala
 290 295 300
 Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly
 305 310 315 320
 Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg
 325 330 335
 Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
 340 345 350
 Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
 355 360 365
 Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
 370 375 380
 Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
 385 390 395 400
 Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
 405 410 415
 Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
 420 425 430
 Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
 435 440 445
 Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
 450 455 460
 Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
 465 470 475 480
 Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
 485 490 495
 Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 19
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 342 bp from *A. thaliana* FAB1 (SEQ ID NO:1) and
 3' 1179 bp from *B. napus* elongase KCS (SEQ ID
 NO:3) having mutations at positions 271, 272, 275
 and 920; designated At114 L91C K92R G307D;
 hypothetical

<221> CDS
 <222> (1) ... (1518)

Met	Asn	acg	tcc	ggt	aac	ggt	aag	ctc	ctt	tac	cgt	tat	gtc	tta	acc	aac	48
Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn		
1				5					10					15			
ttt	ttc	aac	ctc	tgt	ttg	ttc	cgg	tta	acg	gcg	ttc	ctc	gcc	gga	aaa		96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys		
			20					25					30				
gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc		144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu		
		35					40					45					
caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	ggt	ttc		192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe		
		50				55					60						
ggt	ttg	ggt	ctc	tac	atc	gta	acc	cga	ccc	aat	cgg	ggt	tat	ctc	ggt		240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val		
		65			70					75				80			
gac	tac	tcg	tgt	tac	ctt	cgg	cca	cgg	cat	tgc	aga	ggt	agt	gtc	tct		288
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Cys	Arg	Val	Ser	Val	Ser		
				85					90					95			
aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca		336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser		
			100					105					110				
cgg	aac	ggc	acg	tgt	gat	aat	tcg	tcg	ttg	gac	ttc	ttg	agg	aag			384
Arg	Asn	Gly	Thr	Cys	Asp	Asn	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys		
		115				120					125						
att	caa	gaa	cgt	tca	ggt	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg		432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly		
		130				135					140						
ctg	ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag		480
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu		
				145	150					155				160			
acg	gag	caa	ggt	atc	att	ggt	gcg	cta	gaa	aat	cta	ttc	aag	aac	acc		528
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr		
				165				170					175				
aac	ggt	aac	cct	aaa	gat	ata	ggt	ata	ctt	gtg	gtg	aac	tca	agc	atg		576
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met		
			180					185					190				
ttt	aat	cca	act	cca	tcg	ctc	tcc	gcg	atg	gtc	ggt	aac	act	ttc	aag		624
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys		
		195															

gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat 720
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240

aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac 768
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255

att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc 816
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270

cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt 864
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285

aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga 912
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Arg Thr His Thr Gly
 290 295 300

gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac 960
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gly Asp Asp Glu Asn
 305 310 315 320

ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt 1008
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335

cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg 1056
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350

tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt 1104
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365

ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct 1152
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg 1200
 Ile Asp His Phe Cys Ile His Ala Gly Gly Ala Val Ile Asp Val
 385 390 395 400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

tca gag act cgt gtc caa aac ggt cgg tcc taa 1521
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
500 505

<213> Artificial Sequence

<223> 5' 114 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having mutations at positions 91, 92 and 307; designated At114 L91C K92R G307D; hypothetical

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5				10					15		
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
			20					25				30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
			35				40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
			50			55					60				
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65				70						75					80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Cys	Arg	Val	Ser	Val	Ser
			85						90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
			100					105				110			
Arg	Asn	Gly	Thr	Cys	Asp	Asn	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
			115				120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Gly	Thr	His	Gly	Pro	Glu	Gly
			130			135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Gly
145				150						155					160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
			165						170					175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180					185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
			195				200					205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser

210		215		220
Ala Gly Val Ile	Ala Ile Asp	Leu Ala Lys	Asp Leu Leu His	Val His
225	230	235	240	
Lys Asn Thr Tyr	Ala Leu Val Val	Ser Thr Glu Asn	Ile Thr Tyr Asn	
	245	250	255	
Ile Tyr Ala Gly	Asp Asn Arg Ser	Met Met Val Ser	Asn Cys Leu Phe	
260	265	270		
Arg Val Gly Gly	Ala Ala Ile Leu	Leu Ser Asn Lys	Pro Gly Asp Arg	
275	280	285		
Arg Arg Ser Lys	Tyr Glu Leu Val	His Thr Val Arg	Thr His Thr Gly	
290	295	300		
Ala Asp Asp Lys	Ser Phe Arg Cys	Val Gln Gln Gly	Asp Asp Glu Asn	
305	310	315	320	
Gly Lys Ile Gly	Val Ser Leu Ser	Lys Asp Ile Thr	Asp Val Ala Gly	
	325	330	335	
Arg Thr Val Lys	Lys Asn Ile Ala Thr	Leu Gly Pro Leu	Ile Leu Pro	
340	345	350		
Leu Ser Glu Lys	Leu Leu Phe Phe	Val Thr Phe Met	Gly Lys Lys Leu	
355	360	365		
Phe Lys Asp Lys	Ile Lys His Tyr	Tyr Val Pro Asp	Phe Lys Leu Ala	
370	375	380		
Ile Asp His Phe	Cys Ile His Ala	Gly Gly Arg Ala	Val Ile Asp Val	
385	390	395	400	
Leu Glu Lys Asn	Leu Ala Leu Ala	Pro Ile Asp Val	Glu Ala Ser Arg	
	405	410	415	
Ser Thr Leu His	Arg Phe Gly Asn	Thr Ser Ser Ser	Ser Ile Trp Tyr	
420	425	430		
Glu Leu Ala Tyr	Ile Glu Ala Lys	Gly Arg Met Lys	Lys Gly Asn Lys	
435	440	445		
Val Trp Gln Ile	Ala Leu Gly Ser	Gly Phe Lys Cys	Asn Ser Ala Val	
450	455	460		
Trp Val Ala Leu	Asn Asn Val Lys	Ala Ser Thr Asn	Ser Pro Trp Glu	
465	470	475	480	
His Cys Ile Asp	Arg Tyr Pro Val	Lys Ile Asp Ser	Asp Ser Gly Lys	
	485	490	495	
Ser Glu Thr Arg	Val Gln Asn Gly	Arg Ser		
500	505			

<210> 21
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3) having mutations at positions 275 and 920;
 designated At114 K92R G307D; hypothetical

<221> CDS
 <222> (1)...(1518)

<400> 21
 atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

NOBEL PRIZE **FOR** **PEACE**

[illegible]

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<210> 22
<211> 506
<212> PRT
<213> Artificial Sequence
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<220>
<223> 5' 114 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having mutations at positions 92 and 307; designated At114 K92R G307D; hypothetical

400> 22																		
Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn			
1				5				10					15					
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys			
			20					25					30					
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu			
		35					40					45						
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe			
	50					55					60							
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val			
65					70					75					80			
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Arg	Val	Ser	Val	Ser			
			85						90				95					
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser			
			100					105					110					
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys			
		115					120					125						
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly			
	130					135					140							
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu			
145					150					155					160			
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr			
			165						170					175				
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met			
			180					185					190					
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys			
		195					200					205						
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser			
	210					215					220							
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His			
	225			230						235					240			
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn			
			245						250					255				
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe			

260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 23

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 762 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and

3' 759 bp from *B. napus* elongase KCS (SEQ ID
NO:3); designated At254

<221> CDS

<222> (1)...(1518)

<400> 23

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 1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ctc ctt tcc tat ctc 144
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Leu Leu Ser Tyr Leu
 35 40 45

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cgt Arg	ggt Val	ggg Gly	gcc Gly	gct Ala	att Ile	ttg Leu	ctc Leu	tcc Ser	aac Asn	aag Lys	cct Pro	gga Gly	gat Asp	cgt Arg	864		
275															280		
aga Arg	cgg Arg	tcc Ser	aag Lys	tac Tyr	gag Glu	cta Leu	ggt Val	cac His	acg Thr	gtt Val	cga Arg	acg Thr	cat His	acc Thr	gga Gly	912	
290															295		
gct Ala	gac Asp	ggc Gly	aag Lys	tct Ser	ttt Phe	cgt Arg	tgc Cys	gtg Val	caa Gln	caa Gln	gga Gly	gac Asp	gat Asp	gag Glu	aac Asn	960	
305															310	315	320
ggc Gly	aaa Lys	atc Ile	gga Gly	gtg Val	agt Ser	ttg Leu	tcc Ser	aag Lys	gac Asp	ata Ile	acc Thr	gat Asp	ggt Val	gct Ala	ggt Gly	1008	
325															330	335	
cga Arg	acg Thr	ggt Val	aag Lys	aaa Lys	aac Asn	ata Ile	gca Ala	acg Thr	ttg Leu	ggt Gly	ccg Pro	ttg Leu	att Ile	ctt Leu	ccg Pro	1056	
340															345	350	
tta Leu	agc Ser	gag Glu	aaa Lys	ctt Leu	ctt Leu	ttt Phe	ttc Phe	ggt Val	acc Thr	ttc Phe	atg Met	ggc Gly	aag Lys	aaa Lys	ctt Leu	1104	
355															360	365	
ttc Phe	aaa Lys	gat Asp	aaa Lys	atc Ile	aaa Lys	cat His	tac Tyr	tac Tyr	gtc Val	ccg Pro	gat Asp	ttc Phe	aaa Lys	ctt Leu	gct Ala	1152	
370															375	380	
att Ile	gac Asp	cat His	ttt Phe	tgt Cys	ata Ile	cat His	gcc Ala	gga Gly	ggc Gly	aga Arg	gac Ala	gtg Val	att Ile	gat Asp	gtg Val	1200	
385															390	395	400
cta Leu	gag Glu	aag Lys	aac Asn	cta Leu	gcc Ala	cta Leu	gca Ala	ccg Pro	atc Ala	gat Asp	gta Val	gag Glu	gca Ala	tca Ser	aga Arg	1248	
405															410	415	
tca Ser	acg Thr	tta Leu	cat His	aga Arg	ttt Phe	gga Gly	aac Asn	act Thr	tca Ser	tct Ser	agc Ser	tca Ser	ata Ile	tgg Trp	tat Tyr	1296	
420															425	430	
gag Glu	ttg Leu	gca Ala	tac Tyr	ata Ile	gaa Glu	gca Ala	aaa Lys	gga Gly	agg Arg	atg Met	aag Lys	aaa Lys	ggt Gly	aat Asn	aaa Lys	1344	
435															440	445	
ggt Val	tgg Trp	cag Gln	att Ile	gct Ala	tta Leu	ggg Gly	tca Gly	ggc Phe	ttt Lys	aag Lys	tgt Cys	aac Asn	agt Ser	gca Ala	ggt Val	1392	
450															455	460	
tgg Trp	gtg Val	gct Ala	cta Leu	aac Asn	aat Asn	gtc Val	aaa Lys	gct Ala	tcg Ser	aca Thr	aat Asn	agt Pro	cct Pro	tgg Trp	gaa Glu	1440	
465															470	475	480
cac His	tgc Cys	atc Ile	gac Asp	aga Arg	tac Tyr	cgc Pro	gtc Val	aaa Lys	att Ile	gat Asp	tct Ser	gat Asp	tca Ser	ggt Gly	aag Lys	1488	
485															490	495	
tca Gly	gag Ser	act Cys	cgt Gly	gtc Ala	cca Gly	aac Gly	ggg Gly	cgg Gly	tcc Gly	taa Gly						1521	

Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
500 505

<210> 24
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> 5' 254 amino acids from A. thaliana FAE1 (SEQ ID
NO:2) and 3' 252 amino acids from B. napus
elongase KCS (SEQ ID NO:4); designated At254

<400> 24
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Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
20 25 30
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Leu Leu Ser Tyr Leu
35 40 45
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50 55 60
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65 70 75 80
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
85 90 95
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
100 105 110
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
115 120 125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
130 135 140
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
145 150 155 160
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
165 170 175
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
180 185 190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
195 200 205
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
210 215 220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225 230 235 240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
245 250 255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
260 265 270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
275 280 285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
290 295 300
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305 310 315 320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
325 330 335

[illegible]

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 519 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and
3' 1002 bp from *B. napus* elongase KCS (SEQ ID
NO:3); designated At173

<221> CDS

<222> (1) . . . (1518)

<400> 25

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac 48
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1 5 10 15

ttt ttc aac ctc tgt ttg ttc cgg tta acg gcg ttc ctc gcc gga aaa 96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50 55 60

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65 70 75 80

[illegible]

Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320

ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt 1008
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335

cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt cgg 1056
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350

tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt 1104
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365

ttc aaa gat aaa atc aaa cat tac tac gtc cgg gat ttc aaa ctt gct 1152
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg 1200
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400

cta gag aag aac cta gcc cta gca cgg atc gat gta gag gca tca aga 1248
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac cgg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

tca gag act cgt gtc cma aac ggt cgg tcc taa 1521
 Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser
 500 505

<210> 26
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<223> 5' 173 amino acids from A. thaliana PAE1 (SEQ ID NO:2) and 3' 333 amino acids from B. napus elongase KCS (SEQ ID NO:4); designated At173

 $\langle 222 \rangle \quad (0) \dots (0)$

<400> 26

[illegible]

Order by 11:00 AM
Delivery by 12:00 PM

400> 27																
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Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn	48															
1 5 10 15																
96																
ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa																
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys	96															
20 25 30																
144																
gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat																
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr	144															
35 40 45																
192																
ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt																
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val	192															
50 55 60																
240																
ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc																
Phe Gly Ser Val Leu Thr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu	240															
65 70 75 80																
288																
ggt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc																
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile	288															
85 90 95																
336																
tcc aaq qtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct																
	336															

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	325	330	335	
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct				1056
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro				
340		345	350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt				1104
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu				
355		360	365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct				1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala				
370		375	380	
gtt gac cat ttc tgt att cat gcc gga gcc aga gcc gtg atc gat gag				1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu				
385		390	395	400
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga				1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg				
405		410	415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat				1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr				
420		425	430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa				1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys				
435		440	445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt				1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val				
450		455	460	
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa				1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln				
465		470	475	480
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag				1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys				
485		490	495	
tca aag act cat gtc caa aac ggt cgg tcc taa				1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser				
500		505		

<210> 28

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 176 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) and 3' 330 amino acids from *A. thaliana* FAEl (SEQ ID NO:2); designated Bn176

<400> 28

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Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
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20      25      30
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
35      40      45
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
50      55      60
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
65      70      75      80
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
85      90      95
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
100      105      110
Arg Asn Gly Thr Cys Asp Asp Ser Trp Leu Asp Phe Leu Arg Lys
115      120      125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
130      135      140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
145      150      155      160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
165      170      175
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
180      185      190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
195      200      205
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
210      215      220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225      230      235      240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
245      250      255
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
260      265      270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
275      280      285
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
290      295      300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
305      310      315      320
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
325      330      335
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
340      345      350
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
355      360      365
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
370      375      380
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
385      390      395      400
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
405      410      415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
420      425      430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
435      440      445

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100%

<220>
<223> 5' 1197 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and
3' 324 bp from *B. napus* elongase KCS (SEQ ID
NO:3); designated At399

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<222> (1) ... (1518)
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1				5				10						15			
ttt	ttc	aac	ctc	tgt	ttg	ttc	ccg	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96	
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys		
			20					25					30				
gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144	
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu		
			35				40					45					
caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	ggt	ttc	192	
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe		
			50				55				60						
ggt	ttg	gtt	ctc	tac	atc	gta	acc	cga	ccc	aat	ccg	ggt	tat	ctc	ggt	240	
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val		
	65				70					75					80		
gac	tac	tcg	tgt	tac	ctt	cca	cca	ccg	cat	ctc	aaa	ggt	agt	gtc	tct	288	
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser		
				85					90					95			
aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser		
			100					105				110					
cgg	aac	gtg	gca	tgt	gat	gat	ccg	tcc	tcg	ctc	gat	ttc	ctg	agg	aag	384	
Arg	Asn	Val	Ala	Tyr	Asp	Asp	Pro	Ser	Leu	Asp	Phe	Leu	Arg	Gly	Lys		
			115				120					125					
att	caa	gag	cgt	tca	ggt	cta	ggt	gat	gag	acg	tac	agt	cct	gag	gga	432	
Ile	Gln	Gly	Arg	Ser	Gly	Leu	Gly	Asp	Gly	Thr	Tyr	Ser	Pro	Glu	Gly		

[illegible]

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 370 375 380

gtt gac cat ttc tgt att cat gcc gga gcc aga gcc gtg atc gat gtg 1200
 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tgg aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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 Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser
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<210> 30

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 399 amino acids from *A. thaliana* FAEl (SEQ ID
 NO:2) and 3' 107 amino acids from *B. napus*
 elongase KCS (SEQ ID NO:4); designated At399

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Pro or Gln

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 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

Aia	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
Gln	His	35	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
Gly	Leu	50	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu
65	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	His	75	Leu	Lys	Val	Ser	Val
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	90	Lys	Ala	Asp	Thr	Ser
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	105	Leu	Asp	Phe	Leu	Arg
Ile	Gln	115	Glu	Arg	Ser	Gly	Leu	Gly	Asp	120	Glu	Thr	Tyr	Ser	Pro
Leu	Ile	130	His	Val	Pro	Pro	Arg	Lys	Thr	135	Phe	Ala	Ala	Ser	Arg
145	Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	150	Glu	Asn	Leu	Phe	Glu
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	165	Val	Val	Asn	Ser	Ser
Phe	Asn	180	Pro	Thr	Pro	Ser	Leu	Ser	Ala	185	Met	Val	Val	Asn	Thr
Leu	Arg	195	Ser	Asn	Ile	Lys	Ser	Phe	Asn	200	Leu	Gly	Gly	Met	Gly
Ala	Gly	210	Val	Ile	Ala	Ile	Asp	Leu	Ala	215	Lys	Asp	Leu	Leu	His
225	Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Thr	220	Glu	Asn	Ile	Thr	Gln
Ile	Tyr	Ala	Gly	Glu	Asn	Arg	Ser	Met	Met	225	Val	Ser	Asn	Cys	Leu
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	230	Asn	Lys	Ser	Gly	Asp
Arg	Arg	240	Ser	Lys	Tyr	Lys	Leu	Val	His	235	Thr	Val	Arg	Thr	His
Ala	Asp	250	Asp	Lys	Ser	Phe	Arg	Cys	Val	240	Gln	Glu	Asn	Asp	Glu
305	Gly	Lys	Ile	Gly	Val	Cys	Leu	Ser	Lys	245	Asp	Ile	Thr	Asn	Val
Thr	Thr	Leu	Thr	Lys	Asn	Ile	Ala	Thr	Leu	250	Gly	Pro	Leu	Ile	Leu
Leu	Ser	Glu	Lys	Phe	Leu	Phe	Phe	Ala	Thr	255	Phe	Val	Ala	Lys	Lys
Leu	Lys	355	Asp	Lys	Ile	Lys	His	Tyr	Val	360	Pro	Asp	Phe	Lys	Leu
Val	Asp	370	His	Phe	Cys	Ile	His	Ala	Gly	365	Gly	Arg	Ala	Val	Ile
385	Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	370	Ile	Asp	Val	Glu	Ala
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	375	Ser	Ser	Ser	Ser	Ile
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	380	Met	Lys	Lys	Gly	Asn
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	385	Lys	Cys	Asn	Ser	Ala
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	390	Thr	Asn	Ser	Pro	Trp
465	His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	395	Ile	Asp	Ser	Asp	Ser
480										400					

400> 31	atg	acg	tcc	att	aac	gtt	aag	ctc	ctt	tac	cat	tac	gtc	ata	acc	aac	48
Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	Thr	Asn		
1				5				10						15			
ctt	ttc	aac	ctt	tgc	ttc	ttt	cgg	tta	acg	gcg	atc	gtc	gcc	gga	aaa	96	
Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	Gly	Lys		
			20					25					30				
gcc	tat	Cgg	ctt	acc	ata	gac	gat	ctt	cac	cac	tta	tac	tat	tcc	tat	144	
Ala	Tyr	Arg	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr			
		35				40						45					
ctc	caa	cac	aac	ctc	ata	acc	atc	gct	cca	ctc	ttt	gcc	ttc	acc	gtt	192	
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val		
	50					55					60						
ttc	ggt	tcg	gtt	ctc	tac	atc	gca	acc	cgg	ccc	aaa	ccg	gtt	tac	ctc	240	
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu		
65				70						75				80			
gtt	gag	tac	tca	tgc	tac	ctt	cca	cca	acg	cat	tgt	aga	tca	agt	atc	288	
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile		
			85						90				95				
tcc	aag	gtc	atg	gat	atc	ttt	tat	caa	gta	aga	aaa	gct	gat	cct	tct	336	
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser		
			100					105				110					
cgg	aac	ggc	acg	tgc	gat	gac	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag	384	
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys		
		115					120				125						
att	caa	gaa	cgt	tca	ggt	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg	432	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly		
	130					135					140						
ctg	ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	480	
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu		
145				150						155				160			

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc 528
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175

aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg 576
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190

ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag 624
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205

ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt 672
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220

gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat 720
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240

aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac 768
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255

att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc 816
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270

cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt 864
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285

aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga 912
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300

gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac 960
 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320

ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt 1008
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335

cga acg gtt aag aaa aac ata gca acg ttg ggt cgg ttg att ctt cgg 1056
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350

tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt 1104
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365

ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct 1152
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg atc gat gag 1200
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
 385 390 395 400

cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga 1248
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ser Trp Tyr
 420 425 430

gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt 1392
 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa 1440
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
 465 470 475 480

cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
 485 490 495

tca aag act cat gtc caa aac ggt cgg tcc taa 1521
 Ser Lys Thr His Val Gln Asn Gly Arg Ser
 500 505

<210> 32

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 399 amino acids from B. napus elongase KCS (SEQ
 ID NO:3) and 3' 107 amino acids from A. thaliana
 FAE1 (SEQ ID NO:1); designated Bn399

<400> 32

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 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
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 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser

[illegible]

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<210> 33
<211> 1524
<212> DNA
<213> Artificial Sequence
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<223> 1524 bp from *B. napus* elongase KCS (SEQ ID NO:3)
having a mutation at position 920; designated Bn
G307D; hypothetical

<222> (1) ... (1518)

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Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
1 5 10 15

cct ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa 96
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30

gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat 144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
35 40 45

ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt 192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
50 55 60

ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa cgg gtt tac ctc 240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
65 70 75 80

gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc 288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
85 90 95

tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct 336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
100 105 110

cgg aac ggc acg tgc gat gac tcg tgg ctt gac ttc ttg agg aag 384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
115 120 125

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
130 135 140

ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag 480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
145 150 155 160

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc 528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
165 170 175

aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg 576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
180 185 190

ttt Phe	aat Asn	cca Pro	act Thr	cca Pro	tcg Ser	ctc Leu	tcc Ala	gcg Ala	atg Met	gtc Val	gtt Val	aac Asn	act Thr	ttc Phe	aag Lys	624
195 200																
ctc Leu	cga Arg	agc Ser	aac Asn	gta Val	aga Arg	agc Ser	ttt Phe	aac Asn	ctt Leu	ggc Gly	ggc Gly	atg Met	ggc Gly	tgt Cys	agt Ser	672
210 215																
gcc Ala	ggc Gly	gtt Val	ata Ile	gcc Ala	att Ile	gat Asp	cta Leu	gca Ala	aag Lys	gac Asp	ttg Leu	ttg Leu	cat His	gtc Val	cat His	720
225 230																
aaa Lys	aat Asn	acg Thr	tat Thr	gct Ala	ctt Leu	gtg Val	gtg Val	agc Ser	aca Thr	gag Glu	aac Asn	atc Ile	act Thr	tat Cys	aac Asn	768
245 250																
att Ile	tac Tyr	gct Ala	ggc Gly	gat Asp	aat Asn	agg Arg	tcc Ser	atg Met	atg Met	gtt Val	tca Ser	aat Asn	tgc Cys	ttg Leu	ttc Phe	816
260 265																
cgt Arg	gtt Val	ggc Gly	ggg Gly	gcc Ala	gct Ala	att Ile	ttg Leu	ctc Leu	tcc Ser	aac Asn	aag Lys	cct Pro	gga Gly	gat Asp	cgt Arg	864
275 280																
aga Arg	cgg Arg	tcc Ser	aag Lys	tac Tyr	gag Glu	cta Leu	gtt Val	cac His	acg Thr	gtt Val	cga Arg	acg Thr	cat His	acc Thr	gga Gly	912
290 295																
gct Ala	gac Asp	gac Asp	aag Lys	tct Ser	ttt Phe	cgt Arg	tgc Cys	gtg Val	caa Gln	caa Gln	gga Gly	gac Asp	gat Asp	gag Glu	aac Asn	960
305 310																
ggc Gly	aaa Lys	atc Ile	gga Gly	gtg Val	agt Ser	ttg Leu	tcc Ser	aag Lys	gac Asp	ata Ile	acc Thr	gat Asp	gtt Val	gct Ala	ggt Gly	1008
325 330																
cga Arg	acg Thr	gtt Val	aag Lys	aaa Lys	aac Asn	ata Ile	gca Ala	acg Thr	ttg Leu	ggc Gly	ccg Pro	ttg Leu	att Val	ctt Leu	ccg Pro	1056
340 345																
tta Leu	agc Ser	gag Glu	aaa Lys	ctt Leu	ctt Leu	ttt Phe	ttc Phe	gtt Val	acc Thr	ttc Phe	atg Met	ggc Gly	aag Lys	aaa Lys	ctt Leu	1104
355 360																
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370 375																
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385 390																
cta Leu	gag Glu	aag Lys	aac Asn	cta Leu	gcc Ala	cta Leu	gca Ala	ccg Pro	ile Ala	gat Asp	gta Val	gag Glu	gca Ala	tca Ser	aga Arg	1248
405 410																
tca Glu	acg Glu	tta Lys	cat Asn	aga Leu	ttt Leu	gga Ala	aac Leu	act Ala	tca Pro	tct Val	agc Val	tca Glu	ata Ala	tggt Ser	tat Arg	1296

Figure 1. The structure of the proposed model.

Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 35

<211> 1709

<212> DNA

<213> Artificial Sequence

<220>

<223> 1709 bp from *A. thaliana* FAE1 (SEQ ID NO:1) having
 a mutation at position 275; designated At K92R;
 hypothetical

<221> CDS

<222> (1)... (1518)

<400> 35

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 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

gcc tct ccg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80

gac tac tcg tgt tac ctt cca cca ccg cat ctc aga gtt agt gtc tct 288
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser
 85 90 95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110

ccg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag 384
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125

att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
 130 135 140

ctc att cac gta cca ccg ccg aag act ttt gca gcg tca cgt gaa gag 480
 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
 145 150 155 160

aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc 528
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
 165 170 175

aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg 576
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190

ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag 624
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205

ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt 672
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220

gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat 720

Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
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Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly	
245 250 255	
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Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tgc gga gac cgg	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg	
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aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga	912
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly	
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gct gat gac aag tct ttt cga tgt gtg caa caa gaa gac gat gag agc	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Glu Asp Asp Glu Ser	
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Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly	
325 330 335	
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Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
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Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu	
355 360 365	
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Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
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Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu	
385 390 395 400	
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Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
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Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	

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Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
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Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
			20					25				30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50					55				60					
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65				70					75					80	
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Arg	Val	Ser	Val	Ser
			85					90				95			
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
			100					105				110			
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys
			115					120				125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly
	130					135					140				
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu
145					150					155				160	
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr
				165				170					175		
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180					185				190			
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
		195					200					205			
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210					215					220				

Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
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 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
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 Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
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 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
 275 280 285
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 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
 305 310 315 320
 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
 325 330 335
 Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
 355 360 365
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
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 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
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 485 490 495
 Ser Lys Thr His Val Gln Asn Gly Arg Ser
 500 505

<210> 37

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 762 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and
 3' 759 bp from *B. napus* elongase KCS (SEQ ID NO:3)
 and having a mutation at position 920; designated
 At254 G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 37

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 1 5 10 15

48

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa

96

Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
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gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
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Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
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ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
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Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr	
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Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	
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Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
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Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
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gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aac act tat gct ctc gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	

										245										250										255																													
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Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe																																												
																260											265											270																					
cgt	gtt	ggg	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt											864																																	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg																																												
																275											280											285																					
aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga											912																																	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly																																												
																290											295											300																					
gct	gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac											960																																	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn																																												
																305											310											315											320										
ggc	aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggg											1008																																	
Gly	Lys	Ile	Gly	Val	Leu	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly																																											
																325											330											335																					
cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggg	ccg	ttg	att	ctt	ccg											1056																																	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro																																												
																340											345											350																					
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	acc	ttc	atg	ggc	aag	aaa	ctt											1104																																		
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu																																												
																355											360											365																					
ttc	aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct											1152																																	
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala																																												
																370											375											380																					
att	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg											1200																																	
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val																																												
																385											390											395											400										
cta	gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga											1248																																	
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg																																												
																405											410											415																					
tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tgg	tat											1296																																	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr																																												
																420											425											430																					
gag	ttg	gca	tac	ata	gaa	gca	aaa	gga	agg	atg	aag	aaa	ggg	aat	aaa											1344																																	
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys																																												
																435											440											445																					
gtt	tgg	cag	att	gct	tta	ggg	tca	ggc	ttt	aag	tgt	aac	agt	gca	gtt											1392																																	
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val																																												
																450											455											460																					
tgg	gtg	gct	cta	aac	aat	gtc	aaa	gct	tcg	aca	aat	agt	cct	tgg																																													

tca gag act cgt gtc caa aac ggt cgg tcc taa 1521
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
500 505

<220>
<223> 5' 254 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 252 amino acids from B. napus elongase KCS (SEQ ID NO:4) having a mutation at residue 307; designated At254 G307D; hypothetical

400> 38																			
Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn				
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Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys				
			20					25					30						
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu				
			35					40					45						
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe				
			50				55				60								
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val				
65					70					75					80				
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser				
				85					90					95					
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser				
			100					105					110						
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys				
			115				120					125							
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly				
			130				135				140								
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu				
145					150					155					160				
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr				
				165					170					175					
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met				
			180					185					190						
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys				
			195				200					205							
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser				
			210				215				220								
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His				
225					230					235					240				
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn				
				245					250					255					
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe				
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<210> 39
<211> 1521
<212> DNA
<213> Artificial Sequence
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<221> CDS
<222> (1) . . . (1518)

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1				5					10					15		
ttt	ttc	aac	ctc	tgt	ttg	ttc	cgc	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
			20					25					30			
gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
		35					40					45				

192	gln	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	ggt	ttc
	His	50	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	55															
240	ggt	ttg	ggt	ctc	tac	atc	gta	acc	cga	ccc	aat	ccg	ggt	tat	ctc	ggt
	Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
	70															
288	gac	tac	tcg	tgt	tac	ctt	cca	cca	ccg	cat	ctc	aaa	ggt	agt	gtc	tct
	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser
	85															
336	aaa	gtc	atg		att	ttc	tac		caa	ata	aga	aaa	gct	gat	tct	tca
	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
	100															
384	cgg	aac	gtg	gca	tgt	gat	gat	ccg	tcc	tcg	ctc	gat	ttc	ctg	agg	aag
	Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys
	115															
432	att	caa	gag	cgt	tca	ggt	cta	ggt	gat	gag	acg	tac	agt	cct	gag	gga
	Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly
	130															
480	ctc	att	cac	gta	cca	ccg	cgg	aag	act	ttt	gca	gcg	tca	cgt	gaa	gag
	Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu
	145															
528	aca	gag	aag	ggt	atc	atc	ggt	gcg	ctc	gaa	aat	cta	aag	aac	acc	
	Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
	165															
576	aac	ggt	aac	cct	aaa	gat	ata	ggt	ata	ctt	gtg	gtg	aac	tca	agc	atg
	Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
	180															
624	ttt	aat	cca	act	cca	tcg	ctc	tcc	gcg	atg	gtc	ggt	aat	act	ttc	aag
	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
	195															
672	ctc	cga	agc	aac	gta	aga	agc	ttt	aac	ctt	ggt	ggc	atg	ggt	tgt	agt
	Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210															
720	gcc	ggt		ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat
	Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
	230															
768	aaa	aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac
	Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
	245															
816	att	tac	gct	ggt	gat	aat	agg	tcc	atg	atg	ggt	tca	aat	tgc	ttg	ttc
	Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
	260															
864	cgt	ggt	ggt	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aaq	cct	qga	gat	cgt

Arg Val Gly	Gly Ala Ala	Ile Leu Leu	Ser Asn Lys	Pro Gly Asp	Arg	
275		280		285		
aga cgg tcc	aag tac gag	cta gtt cac	acg gtt cga	acg cat acc	gga	912
Arg Arg Ser	Lys Tyr Glu	Leu Val His	Thr Val Arg	Thr His Thr	Gly	
290		295		300		
gct gac gac	aag tct ttt	cgt tgc gtg	caa caa gga	gac gat gag	aac	960
Ala Asp Asp	Lys Ser Phe	Arg Cys Val	Gln Gln Gly	Asp Asp Glu	Asn	
305	310		315	320		
ggc aaa atc	gga gtg agt	ttg tcc aag	gac ata acc	gat gtt gct	ggc	1008
Gly Lys Ile	Gly Val Ser	Leu Ser Lys	Asp Ile Thr	Asp Val Ala	Gly	
	325		330	335		
cga acg gtt	aag aaa aac	ata gca acg	ttg ggt ccg	ttg att ctt	ccg	1056
Arg Thr Val	Lys Lys Asn	Ile Ala Thr	Leu Gly Pro	Leu Ile Leu	Pro	
	340		345	350		
tta agc gag	aaa ctt ctt	ttt ttc gtt	acc ttc atg	ggc aag aaa	ctt	1104
Leu Ser Glu	Lys Leu Leu	Phe Phe Val	Thr Phe Met	Gly Lys Lys	Leu	
	355		360	365		
ttc aaa gat	aaa atc aaa	cat tac tac	gtc ccg gat	ttc aaa ctt	gct	1152
Phe Lys Asp	Lys Ile Lys	His Tyr Tyr	Val Pro Asp	Phe Lys Leu	Ala	
	370		375	380		
att gac cat	ttt tgt ata	cat gcc gga	ggc aga gcc	gtg att gat	gtg	1200
Ile Asp His	Phe Cys Ile	His Ala Gly	Gly Arg Ala	Val Ile Asp	Val	
	385		390	395	400	
cta gag aag	aac cta gcc	cta gca ccg	atc gat gta	gag gca tca	aga	1248
Leu Glu Lys	Asn Leu Ala	Leu Ala Pro	Ile Asp Val	Glu Ala Ser	Arg	
	405		410	415		
tca acg tta	cat aga ttt	gga aac act	tca tct agc	tca ata tgg	tat	1296
Ser Thr Leu	His Arg Phe	Gly Asn Thr	Ser Ser Ser	Ser Ser Ile	Trp Tyr	
	420		425	430		
gag ttg gca	tac ata gaa	gca aaa gga	agg atg aag	aaa ggt aat	aaa	1344
Glu Leu Ala	Tyr Ile Glu	Ala Lys Gly	Arg Met Lys	Gly Asn Lys		
	435		440	445		
gtt tgg cag	att gct tta	ggg tca ggc	ttt aag tgt	aac agt gca	gtt	1392
Val Trp Gln	Ile Ala Leu	Gly Ser Gly	Phe Lys Cys	Asn Ser Ala	Val	
	450		455	460		
tgg gtg gct	cta aac aat	gtc aaa gct	tcg aca aat	agt cct tgg	gaa	1440
Trp Val Ala	Leu Asn Asn	Val Lys Ala	Ser Thr Asn	Ser Pro Trp	Glu	
	465		470	475	480	
cac tgc atc	gac aga tac	ccg gtc aaa	att gat tct	gat tca ggt	aag	1488
His Cys Ile	Asp Arg Tyr	Pro Val Lys	Ile Asp Ser	Asp Ser Gly	Lys	
	485		490	495		
tca gag act	cgt gtc caa	aac ggt cgg	tcc taa			1521
Ser Glu Thr	Arg Val Gln	Asn Gly Arg	Ser			

500

505

<210> 40
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 173 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 333 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having a mutation at residue 307; designated At173 G307D; hypothetical

<400> 40

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Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	20	25	30	
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	35	40	45	
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	50	55	60	
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	65	70	75	80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	85	90	95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	100	105	110	
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	115	120	125	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	130	135	140	
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	145	150	155	160
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	165	170	175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	180	185	190	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	195	200	205	
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	210	215	220	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	225	230	235	240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	245	250	255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	260	265	270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	275	280	285	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	290	295	300	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	305	310	315	320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	325	330	335	

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<210> 41
<211> 1521
<212> DNA
<213> Artificial Sequence
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<221> CDS
<222> (1) . . . (1518)

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85 90 95	
tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct	336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser	
100 105 110	
cgg aac ggc acg tgc gat gac tgc tgc tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tgc ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	

00077476-000001

gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac 960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305 310 315 320

ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt 1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
325 330 335

cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg 1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
340 345 350

tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt 1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
355 360 365

ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct 1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
370 375 380

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg atc gat gag 1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
385 390 395 400

cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga 1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
405 410 415

tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat 1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
420 425 430

gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa 1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
435 440 445

gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt 1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
450 455 460

tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa 1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
465 470 475 480

cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag 1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
485 490 495

tca aag act cat gtc caa aac ggt cgg tcc taa 1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser
500 505

<210> 42

<211> 506

<212> PRT

<213> Artificial Sequence

<223> 5' 399 amino acids from *B. napus* elongase KCS (SEQ ID NO:3) and 3' 107 amino acids from *A. thaliana* FAE1 (SEQ ID NO:1) having a mutation at residue 306; designated Bn399 G307D; hypothetical

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			20					25					30		
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr
		35					40					45			
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val
	50					55					60				
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu
65				70					75						80
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile
			85						90					95	
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser
			100					105					110		
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
		115					120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
	130					135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Gly
145				150					155					160	
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
			165					170						175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180					185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
		195					200					205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210					215					220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225				230					235					240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
			245						250					255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
		260					265						270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
		275					280					285			
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290					295					300				
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305				310					315					320	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325						330					335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
			340					345					350		
Leu	Ser	Glu	Lys	Leu											

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385          390          395          400
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
          405          410          415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
          420          425          430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
          435          440          445
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
          450          455          460
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
          465          470          475          480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
          485          490          495
Ser Lys Thr His Val Gln Asn Gly Arg Ser
          500          505

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<213> Artificial Sequence

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<220>
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25

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<220>
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33

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<220>
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28

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<220>
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28

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23

<210> 48
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23

<210> 49
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<220>
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<210> 52
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 52
 agagacacta actctgagat gcggtgg 27

<210> 53
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 <212> DNA
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<220>
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<210> 54
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 <212> DNA
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<220>
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<400> 54
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<210> 55
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 <213> Artificial Sequence

<220>
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<210> 56
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 <212> DNA
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<220>
 <223> primer for PCR

<400> 56
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